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<120> MODULATORS OF LEUKOCYTE ACTIVATION, COMPOSITIONS AND METHODS OF USE

<130> A-70224/RMS/DHR

<140> US 10/039,761

<141> 2001-10-19

<150> US 60/280,698

<151> 2001-03-29

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 3955

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1473)..(1473)

<223> "n" at position 1473 can be any base.

<220>

<221> CDS

<222> (355)..(3522)

<223>

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cccgccgtcc tccgccccct catggcccg ggccgcgg acgagcggcg ctgaggcggg 120

ccgcgtggag acgtgaggcg gccgcgtgg ccctcacagt cggcgtttcg ccgcctgccc 180

gcggtgcccg cgcacgcctg cccatcgcc ttgcgcct ggctggcg ggccgtgtcc 240

tcccaaggccg tccgcgccgc tccctggagc tcggcggagc gcggcagcca gggccggcg 300

aggcgcgagg agccggcgcc cacccggcc gccgcggccg cggcgccggg ggcc atg 357
Met

1

acc gtg gag cag aac gtg ctg cag cag agc gcg gcg cag aag cac cag 405
Thr Val Glu Gln Asn Val Leu Gln Ser Ala Ala Gln Lys His Gln

5

10

15

cag acg ttt ttg aat caa ctg aga gaa att acg ggg att aat gac acc 453
Gln Thr Phe Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile Asn Asp Thr

20

25

30

cag ata cta cag caa gcc ttg aag gat agt aat gga aac ttg gaa tta Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu Leu	501
35 40 45	
gca gtg gct ttc ctt act gcg aag aat gct aag acc cct cag cag gag Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln Glu	549
50 55 60 65	
gag aca act tac tac caa aca gca ctt cct ggc aat gat aga tac atc Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr Ile	597
70 75 80	
agt gtg gga agc caa gca gat aca aat gtg att gat ctc act gga gat Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly Asp	645
85 90 95	
gat aaa gat gat ctt cag aga aca att gcc ttg agt ttg gcc gaa tca Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu Ser	693
100 105 110	
aac agg gca ttc agg gag act gga ata act gat gag gaa caa gcc att Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala Ile	741
115 120 125	
agc aga gtt ctt gaa gcc agt ata gca gag aat aaa gca tgt ttg aag Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu Lys	789
130 135 140 145	
agg aca cct aca gaa gtt tgg agg gat tct cga aac cct tat gat aga Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp Arg	837
150 155 160	
aaa aga cag gac aaa gct ccc gtt ggg cta aag aat gtt ggc aat act Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn Thr	885
165 170 175	
tgt tgg ttt agt gct gtt att cag tca tta ttt aat ctt ttg gaa ttt Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu Phe	933
180 185 190	
aga aga tta gtt ctg aat tac aag cct cca tca aat gct caa gat tta Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp Leu	981
195 200 205	
ccc cga aac caa aag gaa cat cgg aat ttg cct ttt atg cgt gag ctg Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu Leu	1029
210 215 220 225	
agg tat cta ttt gca ctt ctt gtt ggt acc aaa agg aag tat gtt gat Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val Asp	1077
230 235 240	
cca tca aga gca gtt gaa att ctt aag gat gct ttc aaa tca aat gac Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn Asp	1125
245 250 255	

tca cag caa gat gtg agt gag ttt aca cac aaa tta tta gat tgg		1173
Ser Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp Trp		
260	265	270
tta gaa gat gcc ttc caa atg aaa gct gaa gag gag acg gat gaa gag		1221
Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu Glu		
275	280	285
aag cca aag aac ccc atg gta gag ttg ttc tat ggc aga ttc ctg gct		1269
Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu Ala		
290	295	300
305		
gtg gga gta ctt gaa ggt aaa aaa ttt gaa aac act gaa atg ttt ggt		1317
Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe Gly		
310	315	320
cag tac cca ctt cag gtc aat ggg ttc aaa gat ctg cat gag tgc cta		1365
Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys Leu		
325	330	335
gaa gct gca atg att gaa gga gaa att gag tct tta cat tca gag aat		1413
Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu Asn		
340	345	350
tca gga aaa tca ggc caa gag cat tgg ttt act gga tta cca cct gtg		1461
Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro Val		
355	360	365
tta aca ttt gan ttg tca aga ttt gaa ttt aat cag gca ttg gga aga		1509
Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly Arg		
370	375	380
385		
cca gaa aaa att cac aac aaa tta gaa ttt ccc caa gtt tta tat ttg		1557
Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr Leu		
390	395	400
405		
gac aga tac atg cac aga aac aga gaa ata aca aga att aag agg gaa		1605
Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg Glu		
410		
415		
gag atc aag aga ctg aaa gat tac ctc acg gta tta caa caa agg cta		1653
Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg Leu		
420	425	430
435		
440		
445		
gaa aga tat tta agc tat ggt tcc ggt ccc aaa cga ttc ccc ttg gta		1701
Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu Val		
455		
460		
465		
gat gtt ctt cag tat gca ttg gaa ttt gcc tca agt aaa cct gtt tgc		1749
Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val Cys		
450	455	460
465		
act tct cct gtt gac gat att gac gct agt tcc cca cct agt ggt tcc		1797
Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly Ser		
470	475	480
485		
ata cca tca cag aca tta cca agc aca aca gaa caa cag gga gcc cta		1845

Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala Leu			
485	490	495	
tct tca gaa ctg cca agc aca tca cct tca tca gtt gct gcc att tca			1893
Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile Ser			
500	505	510	
tcg aga tca gta ata cac aaa cca ttt act cag tcc cggttata cct cca			1941
Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro Pro			
515	520	525	
gat ttg ccc atg cat ccg gca cca agg cac ata acg gag gaa gaa ctt			1989
Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu Leu			
530	535	540	545
tct gtg ctg gaa agt tgt tta cat cgc tgg agg aca gaa ata gaa aat			2037
Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu Asn			
550	555	560	
gac acc aga gat ttg cag gaa agc ata tcc aga atc cat cga aca att			2085
Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr Ile			
565	570	575	
gaa tta atg tac tct gac aaa tct atg ata caa gtt cct tat cga tta			2133
Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg Leu			
580	585	590	
cat gcc gtt tta gtt cac gaa ggc caa gct aat gct ggg cac tac tgg			2181
His Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr Trp.			
595	600	605	
gca tat att ttt gat cat cgt gaa agc aga tgg atg aag tac aat gat			2229
Ala Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn Asp			
610	615	620	625
att gct gtg aca aaa tca tca tgg gaa gag cta gtg agg gac tct ttt			2277
Ile Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser Phe			
630	635	640	
ggt ggt tat aga aat gcc agt gca tac tgt tta atg tac ata aat gat			2325
Gly Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn Asp			
645	650	655	
aag gca cag ttc cta ata caa gag gag ttt aat aaa gaa act ggg cag			2373
Lys Ala Gln Phe Leu Ile Gln Glu Glu Phe Asn Lys Glu Thr Gly Gln			
660	665	670	
ccc ctt gtt ggt ata gaa aca tta cca ccg gat ttg aga gat ttt gtt			2421
Pro Leu Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe Val			
675	680	685	
gag gaa gac aac caa cga ttt gaa aaa gaa cta gaa gaa tgg gat gca			2469
Glu Glu Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Trp Asp Ala			
690	695	700	705
caa ctt gcc cag aaa gct ttg cag gaa aag ctt tta gcg tct cag aaa			2517
Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln Lys			

710	715	720	
ttg aga gag tca gag act tct gtg aca aca gca caa gca gca gga gac Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly Asp 725	730	735	2565
cca gaa tat cta gag cag cca tca aga agt gat ttc tca aag cac ttg Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His Leu 740	745	750	2613
aaa gaa gaa act att caa ata att acc aag gca tca cat gag cat gaa Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His Glu 755	760	765	2661
gat aaa agt cct gaa aca gtt ttg cag tcg gca att aag ttg gaa tat Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu Tyr 770	775	780	2709
785			
gca agg ttg gtt aag ttg gcc caa gaa gac acc cca cca gaa acc gat Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr Asp 790	795	800	2757
tat cgt tta cat cat gta gtg gtc tac ttt atc cag aac cag gca cca Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala Pro 805	810	815	2805
Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg Asn 820	825	830	2853
ttg agt ttt gat gaa agg tgt cac aac ata atg aaa gtt gct caa gcc Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln Ala 835	840	845	2901
aaa ctg gaa atg ata aaa cct gaa gaa gta aac ttg gag gaa tat gag Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr Glu 850	855	860	2949
865			
gag tgg cat cag gat tat agg aaa ttc agg gaa aca act atg tat ctc Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr Leu 870	875	880	2997
ata att ggg cta gaa aat ttt caa aga gaa agt tat ata gat tcc ttg Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser Leu 885	890	895	3045
ctg ttc ctc atc tgt gct tat cag aat aac aaa gaa ctc ttg tct aaa Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser Lys 900	905	910	3093
ggc tta tac aga gga cat gat gaa gaa ttg ata tca cat tat aga aga Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg Arg 915	920	925	3141
gaa tgt ttg cta aaa tta aat gag caa gcc gca gaa ctc ttc gaa tct Glu Cys Leu Leu Lys Leu Asn Glu Gln Ala Ala Glu Leu Phe Glu Ser 930	935	940	3189
		945	

gga gag gat cga gaa gta aac aat ggt ttg att atc atg aat gag ttt		3237
Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile Ile Met Asn Glu Phe		
950	955	960
att gtc cca ttt ttg cca tta tta ctg gtg gat gaa atg gaa gaa aag		3285
Ile Val Pro Phe Leu Pro Leu Leu Leu Val Asp Glu Met Glu Glu Lys		
965	970	975
gat ata cta gct gta gaa gat atg aga aat cga tgg tgt tcc tac ctt		3333
Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg Trp Cys Ser Tyr Leu		
980	985	990
ggt caa gaa atg gaa cca cac ctc caa gaa aag ctg aca gat ttt ttg		3381
Gly Gln Glu Met Glu Pro His Leu Gln Glu Lys Leu Thr Asp Phe Leu		
995	1000	1005
cca aaa ctg ctt gat tgt tct atg gag att aaa agt ttc cat gag		3426
Pro Lys Leu Leu Asp Cys Ser Met Glu Ile Lys Ser Phe His Glu		
1010	1015	1020
cca ccg aag tta cct tca tat tcc acg cat gaa ctc tgt gag cga		3471
Pro Pro Lys Leu Pro Ser Tyr Ser Thr His Glu Leu Cys Glu Arg		
1025	1030	1035
ttt gcc cga atc atg ttg tcc ctc agt cga act cct gct gat gga		3516
Phe Ala Arg Ile Met Leu Ser Leu Ser Arg Thr Pro Ala Asp Gly		
1040	1045	1050
aga taa actgcacact ttccctgaac acactgtata aactttttt agttcttaac		3572
Arg		
1055		
ccttgcccttc ctgtcacagg gtttgcttgt tgctgtata gtttttaact tttttttatt		3632
ttaataactg caaaaagacaa aatgactata cagactttag tcagactgca gacaataaag		3692
ctgaaaatcg catggcgctc agacattta accggaactg atgtataatc acaaatctaa		3752
ttgattttat tatggaaaaa ctatgtttt gccaccctcc tggcgttgcata ttactttgct		3812
tttatctttt ctttctcaac agctttccat tcagtttttttgcata actacagccaa		3872
tttaagtgtt cagcactgtg tacgatacat aatatttggt agttgtaaa tgaaataaag		3932
aataaaagttt tatttatggc tac		3955

<210> 2
 <211> 1055
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (373)..(373)
 <223> The 'Xaa' at location 373 stands for Glu, or Asp.

<220>
<221> misc_feature
<222> (1473)..(1473)
<223> "n" at position 1473 can be any base.

<400> 2

Met Thr Val Glu Gln Asn Val Leu Gln Gln Ser Ala Ala Gln Lys His
1 5 10 15

Gln Gln Thr Phe Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile Asn Asp
20 25 30

Thr Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu
35 40 45

Leu Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln
50 55 60

Glu Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr
65 70 75 80

Ile Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly
85 90 95

Asp Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu
100 105 110

Ser Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala
115 120 125

Ile Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu
130 135 140

Lys Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp
145 150 155 160

Arg Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn
165 170 175

Thr Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu
180 185 190

Phe Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp

195	200	205
Leu Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu		
210	215	220
Leu Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val		
225	230	235
Asp Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn		
245	250	255
Asp Ser Gln Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp		
260	265	270
Trp Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu		
275	280	285
Glu Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu		
290	295	300
Ala Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe		
305	310	315
Gly Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys		
325	330	335
Leu Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu		
340	345	350
Asn Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro		
355	360	365
Val Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly		
370	375	380
Arg Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr		
385	390	395
Leu Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg		
405	410	415
Glu Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg		
420	425	430

Leu Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu
435 440 445

Val Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val
450 455 460

Cys Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly
465 470 475 480

Ser Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala
485 490 495

Leu Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile
500 505 510

Ser Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro
515 520 525

Pro Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu
530 535 540

Leu Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu
545 550 555 560

Asn Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr
565 570 575

Ile Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg
580 585 590

Leu His Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr
595 600 605

Trp Ala Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn
610 615 620

Asp Ile Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser
625 630 635 640

Phe Gly Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn
645 650 655

Asp Lys Ala Gln Phe Leu Ile Gln Glu Glu Phe Asn Lys Glu Thr Gly
660 665 670

Gln Pro Leu Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe
675 680 685

Val Glu Glu Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Trp Asp
690 695 700

Ala Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln
705 710 720

Lys Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly
725 730 735

Asp Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His
740 745 750

Leu Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His
755 760 765

Glu Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu
770 775 780

Tyr Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr
785 790 795 800

Asp Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala
805 810 815

Pro Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg
820 825 830

Asn Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln
835 840 845

Ala Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr
850 855 860

Glu Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr
865 870 875 880

Leu Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser
885 890 895

Leu Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser
900 905 910

Lys Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg
915 920 925

Arg Glu Cys Leu Leu Lys Leu Asn Glu Gln Ala Ala Glu Leu Phe Glu
930 935 940

Ser Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile Ile Met Asn Glu
945 950 955 960

Phe Ile Val Pro Phe Leu Pro Leu Leu Val Asp Glu Met Glu Glu
965 970 975

Lys Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg Trp Cys Ser Tyr
980 985 990

Leu Gly Gln Glu Met Glu Pro His Leu Gln Glu Lys Leu Thr Asp Phe
995 1000 1005

Leu Pro Lys Leu Leu Asp Cys Ser Met Glu Ile Lys Ser Phe His
1010 1015 1020

Glu Pro Pro Lys Leu Pro Ser Tyr Ser Thr His Glu Leu Cys Glu
1025 1030 1035

Arg Phe Ala Arg Ile Met Leu Ser Leu Ser Arg Thr Pro Ala Asp
1040 1045 1050

Gly Arg
1055

<210> 3
<211> 4015
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1473)..(1473)
<223> "n" at position 1473 can be any base.

<220>
<221> CDS
<222> (355) .. (3582)
<223>

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cccgccgtcc tccgccccgtt catggcccgg gccgccccgg acgagcggcg ctgaggcggg	120	
ccgcgtggag acgtgaggcg gccgccccgtgg ccctcacagt cggcggttcg cgcctgccc	180	
gcgggtgcccgg cgacgcctg ccgcacatcgcc ctgcgcgcct ggctggcggg ggccgtgtcc	240	
tcccaaggccg tccgcgcgc tccctggagc tcggcggagc gcggcagcca gggccggcgg	300	
aggcgcgagg agccggggcgc caccgcgcgc gccgcgcgc cgcgcgcggg ggcc atg	357	
Met		
1		
acc gtg gag cag aac gtg ctg cag cag agc gcg gcg cag aag cac cag	405	
Thr Val Glu Gln Asn Val Leu Gln Gln Ser Ala Ala Gln Lys His Gln		
5 10 15		
cag acg ttt ttg aat caa ctg aga gaa att acg ggg att aat gac acc	453	
Gln Thr Phe Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile Asn Asp Thr		
20 25 30		
cag ata cta cag caa gcc ttg aag gat agt aat gga aac ttg gaa tta	501	
Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu Leu		
35 40 45		
gca gtg gct ttc ctt act gcg aag aat gct aag acc cct cag cag gag	549	
Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln Glu		
50 55 60 65		
gag aca act tac tac caa aca gca ctt cct ggc aat gat aga tac atc	597	
Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr Ile		
70 75 80		
agt gtg gga agc caa gca gat aca aat gtg att gat ctc act gga gat	645	
Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly Asp		
85 90 95		
gat aaa gat gat ctt cag aga aca att gcc ttg agt ttg gcc gaa tca	693	
Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu Ser		
100 105 110		
aac agg gca ttc agg gag act gga ata act gat gag gaa caa gcc att	741	
Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala Ile		
115 120 125		
agc aga gtt ctt gaa gcc agt ata gca gag aat aaa gca tgt ttg aag	789	
Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu Lys		

130	135	140	145	
agg aca cct aca gaa gtt tgg agg gat tct cga aac cct tat gat aga Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp Arg				837
150		155	160	
aaa aga cag gac aaa gct ccc gtt ggg cta aag aat gtt ggc aat act Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn Thr				885
165	170		175	
tgt tgg ttt agt gct gtt att cag tca tta ttt aat ctt ttg gaa ttt Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu Phe				933
180	185		190	
aga aga tta gtt ctg aat tac aag cct cca tca aat gct caa gat tta Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp Leu				981
195	200	205		
ccc cga aac caa aag gaa cat cgg aat ttg cct ttt atg cgt gag ctg Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu Leu				1029
210	215	220	225	
agg tat cta ttt gca ctt ctt gtt ggt acc aaa agg aag tat gtt gat Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val Asp				1077
230	235		240	
cca tca aga gca gtt gaa att ctt aag gat gct ttc aaa tca aat gac Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn Asp				1125
245	250		255	
tca cag cag caa gat gtg agt gag ttt aca cac aaa tta tta gat tgg Ser Gln Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp Trp				1173
260	265		270	
tta gaa gat gcc ttc caa atg aaa gct gaa gag gag acg gat gaa gag Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu Glu				1221
275	280	285		
aag cca aag aac ccc atg gta gag ttg ttc tat ggc aga ttc ctg gct Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu Ala				1269
290	295	300	305	
gtg gga gta ctt gaa ggt aaa aaa ttt gaa aac act gaa atg ttt ggt Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe Gly				1317
310	315		320	
cag tac cca ctt cag gtc aat ggg ttc aaa gat ctg cat gag tgc cta Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys Leu				1365
325	330		335	
gaa gct gca atg att gaa gga gaa att gag tct tta cat tca gag aat Glu Ala Ala Met Ile Glu Gly Ile Glu Ser Leu His Ser Glu Asn				1413
340	345		350	
tca gga aaa tca ggc caa gag cat tgg ttt act gga tta cca cct gtg Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro Val				1461
355	360		365	

tta aca ttt gan ttg tca aga ttt gaa ttt aat cag gca ttg gga aga Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly Arg 370 375 380 385	1509
cca gaa aaa att cac aac aaa tta gaa ttt ccc caa gtt tta tat ttg Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr Leu 390 395 400	1557
gac aga tac atg cac aga aac aga gaa ata aca aga att aag agg gaa Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg Glu 405 410 415	1605
gag atc aag aga ctg aaa gat tac ctc acg gta tta caa caa agg cta Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg Leu 420 425 430	1653
gaa aga tat tta agc tat ggt tcc ggt ccc aaa cga ttc ccc ttg gta Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu Val 435 440 445	1701
gat gtt ctt cag tat gca ttg gaa ttt gcc tca agt aaa cct gtt tgc Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val Cys 450 455 460 465	1749
act tct cct gtt gac gat att gac gct agt tcc cca cct agt ggt tcc Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly Ser 470 475 480	1797
ata cca tca cag aca tta cca agc aca aca gaa caa cag gga gcc cta Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala Leu 485 490 495	1845
tct tca gaa ctg cca agc aca tca cct tca tca gtt gct gcc att tca Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile Ser 500 505 510	1893
tcg aga tca gta ata cac aaa cca ttt act cag tcc cgg ata cct cca Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro Pro 515 520 525	1941
gat ttg ccc atg cat ccg gca cca agg cac ata acg gag gaa gaa ctt Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu Leu 530 535 540 545	1989
tct gtg ctg gaa agt tgt tta cat cgc tgg agg aca gaa ata gaa aat Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu Asn 550 555 560	2037
gac acc aga gat ttg cag gaa agc ata tcc aga atc cat cga aca att Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr Ile 565 570 575	2085
gaa tta atg tac tct gac aaa tct atg ata caa gtt cct tat cga tta Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg Leu 580 585 590	2133

cat gcc gtt tta gtt cac gaa ggc caa gct aat gct ggg cac tac tgg His Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr Trp 595 600 605	2181
gca tat att ttt gat cat cgt gaa agc aga tgg atg aag tac aat gat Ala Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn Asp 610 615 620 625	2229
att gct gtg aca aaa tca tca tgg gaa gag cta gtg agg gac tct ttt Ile Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser Phe 630 635 640	2277
ggt ggt tat aga aat gcc agt gca tac tgt tta atg tac ata aat gat Gly Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn Asp 645 650 655	2325
aag gca cag ttc cta ata caa gag gag ttt aat aaa gaa act ggg cag Lys Ala Gln Phe Leu Ile Gln Glu Glu Phe Asn Lys Glu Thr Gly Gln 660 665 670	2373
ccc ctt gtt ggt ata gaa aca tta cca ccg gat ttg aga gat ttt gtt Pro Leu Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe Val 675 680 685	2421
gag gaa gac aac caa cga ttt gaa aaa gaa cta gaa gaa tgg gat gca Glu Glu Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Trp Asp Ala 690 695 700 705	2469
caa ctt gcc cag aaa gct ttg cag gaa aag ctt tta gcg tct cag aaa Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln Lys 710 715 720	2517
ttg aga gag tca gag act tct gtg aca aca gca caa gca gga gac Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly Asp 725 730 735	2565
cca gaa tat cta gag cag cca tca aga agt gat ttc tca aag cac ttg Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His Leu 740 745 750	2613
aaa gaa gaa act att caa ata att acc aag gca tca cat gag cat gaa Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His Glu 755 760 765	2661
gat aaa agt cct gaa aca gtt ttg cag tcg gca att aag ttg gaa tat Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu Tyr 770 775 780 785	2709
gca agg ttg gtt aag ttg gcc caa gaa gac acc cca cca gaa acc gat Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr Asp 790 795 800	2757
tat cgt tta cat cat gta gtg gtc tac ttt atc cag aac cag gca cca Tyr Arg Leu His His Val Val Tyr Phe Ile Gln Asn Gln Ala Pro 805 810 815	2805
aag aaa att att gag aaa aca tta cta gaa caa ttt gga gat aga aat	2853

Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg Asn			
820	825	830	
ttg agt ttt gat gaa agg tgt cac aac ata atg aaa gtt gct caa gcc			2901
Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln Ala			
835	840	845	
aaa ctg gaa atg ata aaa cct gaa gaa gta aac ttg gag gaa tat gag			2949
Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr Glu			
850	855	860	865
gag tgg cat cag gat tat agg aaa ttc agg gaa aca act atg tat ctc			2997
Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr Leu			
870	875	880	
ata att ggg cta gaa aat ttt caa aga gaa agt tat ata gat tcc ttg			3045
Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser Leu			
885	890	895	
ctg ttc ctc atc tgt gct tat cag aat aac aaa gaa ctc ttg tct aaa			3093
Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser Lys			
900	905	910	
ggc tta tac aga gga cat gat gaa gaa ttg ata tca cat tat aga aga			3141
Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg Arg			
915	920	925	
gaa tgt ttg cta atc ctt aat tta aaa agg aaa caa aaa cct att ctt			3189
Glu Cys Leu Leu Ile Leu Asn Leu Lys Arg Lys Gln Lys Pro Ile Leu			
930	935	940	945
ttt ttt ttc ctg cat tgc att aag aaa tta aat gag caa gca gaa			3237
Phe Phe Leu His Cys Ile Lys Lys Leu Asn Glu Gln Ala Ala Glu			
950	955	960	
ctc ttc gaa tct gga gag gat cga gaa gta aac aat ggt ttg att atc			3285
Leu Phe Glu Ser Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile Ile			
965	970	975	
atg aat gag ttt att gtc cca ttt ttg cca tta ctg gtg gat gaa			3333
Met Asn Glu Phe Ile Val Pro Phe Leu Pro Leu Leu Val Asp Glu			
980	985	990	
atg gaa gaa aag gat ata cta gct gta gaa gat atg aga aat cga tgg			3381
Met Glu Glu Lys Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg Trp			
995	1000	1005	
tgt tcc tac ctt ggt caa gaa atg gaa cca cac ctc caa gaa aag			3426
Cys Ser Tyr Leu Gly Gln Glu Met Glu Pro His Leu Gln Glu Lys			
1010	1015	1020	
ctg aca gat ttt ttg cca aaa ctg ctt gat tgt tct atg gag att			3471
Leu Thr Asp Phe Leu Pro Lys Leu Leu Asp Cys Ser Met Glu Ile			
1025	1030	1035	
aaa agt ttc cat gag cca ccg aag tta cct tca tat tcc acg cat			3516
Lys Ser Phe His Glu Pro Pro Lys Leu Pro Ser Tyr Ser Thr His			

1040	1045	1050	
gaa ctc tgt gag cga ttt	gcc cga atc atg ttg	tcc ctc agt cga	3561
Glu Leu Cys Glu Arg Phe	Ala Arg Ile Met Leu	Ser Leu Ser Arg	
1055	1060	1065	

act cct gct gat gga aga	taa actgcacact ttccctgaac acactgtata	3612
Thr Pro Ala Asp Gly Arg		
1070	1075	

aactctttt agttcttaac cttgccttc ctgtcacagg gtttgcttgt tgctgtata	3672
gtttttaact ttttttatt ttaataactg caaaagacaa aatgactata cagactttag	3732
tcagactgca gacaataaaag ctgaaaatcg catggcgctc agacattta accggaactg	3792
atgtataatc acaaatctaa ttgattttat tatggaaaaa ctatgcttt gccaccctcc	3852
tgttgcatgt ttactttgct tttatctttt ctttctcaac agctttccat tcagtctgga	3912
tccttccatg actacagcca tttaagtgtt cagcactgtg tacgatacat aatatttggt	3972
agcttgtaaa tgaaataaaag aataaagttt tatttatggc tac	4015

<210> 4

<211> 1075

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (373)..(373)

<223> The 'Xaa' at location 373 stands for Glu, or Asp.

<220>

<221> misc_feature

<222> (1473)..(1473)

<223> "n" at position 1473 can be any base.

<400> 4

Met Thr Val Glu Gln Asn Val Leu Gln Gln Ser Ala Ala Gln Lys His		
1	5	10
		15

Gln Gln Thr Phe Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile Asn Asp		
20	25	30

Thr Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu		
35	40	45

Leu Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln		
50	55	60

Glu Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr
65 70 75 80

Ile Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly
85 90 95

Asp Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu
100 105 110

Ser Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala
115 120 125

Ile Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu
130 135 140

Lys Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp
145 150 155 160

Arg Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn
165 170 175

Thr Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu
180 185 190

Phe Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp
195 200 205

Leu Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu
210 215 220

Leu Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val
225 230 235 240

Asp Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn
245 250 255

Asp Ser Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp
260 265 270

Trp Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu
275 280 285

Glu Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu
290 295 300

Ala Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe
305 310 315 320

Gly Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys
325 330 335

Leu Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu
340 345 350

Asn Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro
355 360 365

Val Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly
370 375 380

Arg Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr
385 390 395 400

Leu Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg
405 410 415

Glu Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg
420 425 430

Leu Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu
435 440 445

Val Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val
450 455 460

Cys Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly
465 470 475 480

Ser Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala
485 490 495

Leu Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile
500 505 510

Ser Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro

515	520	525
Pro Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu		
530	535	540
Leu Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu		
545	550	555
Asn Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr		
565	570	575
Ile Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg		
580	585	590
Leu His Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr		
595	600	605
Trp Ala Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn		
610	615	620
Asp Ile Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser		
625	630	635
Phe Gly Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn		
645	650	655
Asp Lys Ala Gln Phe Leu Ile Gln Glu Glu Phe Asn Lys Glu Thr Gly		
660	665	670
Gln Pro Leu Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe		
675	680	685
Val Glu Glu Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Trp Asp		
690	695	700
Ala Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln		
705	710	715
Lys Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly		
725	730	735
Asp Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His		
740	745	750

Leu Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His
755 760 765

Glu Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu
770 775 780

Tyr Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr
785 790 795 800

Asp Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala
805 810 815

Pro Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg
820 825 830

Asn Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln
835 840 845

Ala Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr
850 855 860

Glu Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr
865 870 875 880

Leu Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser
885 890 895

Leu Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser
900 905 910

Lys Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg
915 920 925

Arg Glu Cys Leu Leu Ile Leu Asn Leu Lys Arg Lys Gln Lys Pro Ile
930 935 940

Leu Phe Phe Phe Leu His Cys Ile Lys Lys Leu Asn Glu Gln Ala Ala
945 950 955 960

Glu Leu Phe Glu Ser Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile
965 970 975

Ile Met Asn Glu Phe Ile Val Pro Phe Leu Pro Leu Leu Leu Val Asp
980 985 990

Glu Met Glu Glu Lys Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg
995 1000 1005

Trp Cys Ser Tyr Leu Gly Gln Glu Met Glu Pro His Leu Gln Glu
1010 1015 1020

Lys Leu Thr Asp Phe Leu Pro Lys Leu Leu Asp Cys Ser Met Glu
1025 1030 1035

Ile Lys Ser Phe His Glu Pro Pro Lys Leu Pro Ser Tyr Ser Thr
1040 1045 1050

His Glu Leu Cys Glu Arg Phe Ala Arg Ile Met Leu Ser Leu Ser
1055 1060 1065

Arg Thr Pro Ala Asp Gly Arg
1070 1075

<210> 5
<211> 1075
<212> PRT
<213> Homo sapiens

<400> 5

Met Thr Val Glu Gln Asn Val Leu Gln Gln Ser Ala Ala Gln Lys His
1 5 10 15

Gln Gln Thr Phe Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile Asn Asp
20 25 30

Thr Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu
35 40 45

Leu Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln
50 55 60

Glu Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr
65 70 75 80

Ile Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly

85	90	95
Asp Asp Lys Asp Asp Leu Gln Arg Ala Ile Ala Leu Ser Leu Ala Glu		
100	105	110
Ser Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala		
115	120	125
Ile Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu		
130	135	140
Lys Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp		
145	150	155
160		
Arg Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn		
165	170	175
Thr Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu		
180	185	190
Phe Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp		
195	200	205
Leu Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu		
210	215	220
Leu Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val		
225	230	235
240		
Asp Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn		
245	250	255
Asp Ser Gln Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp		
260	265	270
Trp Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu		
275	280	285
Glu Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu		
290	295	300
Ala Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe		
305	310	315
320		

Gly Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys
325 330 335

Leu Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu
340 345 350

Asn Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Glu Leu Pro Pro
355 360 365

Val Leu Thr Phe Glu Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly
370 375 380

Arg Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr
385 390 395 400

Leu Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg
405 410 415

Glu Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg
420 425 430

Leu Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu
435 440 445

Val Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val
450 455 460

Cys Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly
465 470 475 480

Ser Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala
485 490 495

Leu Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile
500 505 510

Ser Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro
515 520 525

Pro Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu
530 535 540

Leu Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu
545 550 555 560

Asn Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr
565 570 575

Ile Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg
580 585 590

Leu His Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr
595 600 605

Trp Ala Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn
610 615 620

Asp Ile Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser
625 630 635 640

Phe Gly Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn
645 650 655

Asp Lys Ala Gln Phe Leu Ile Gln Glu Glu Phe Asn Lys Glu Thr Gly
660 665 670

Gln Pro Leu Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe
675 680 685

Val Glu Glu Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Glu Trp Asp
690 695 700

Ala Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln
705 710 715 720

Lys Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly
725 730 735

Asp Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His
740 745 750

Leu Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His
755 760 765

Glu Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu
770 775 780

Tyr Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr
785 790 795 800

Asp Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala
805 810 815

Pro Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg
820 825 830

Asn Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln
835 840 845

Ala Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr
850 855 860

Glu Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr
865 870 875 880

Leu Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser
885 890 895

Leu Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser
900 905 910

Lys Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg
915 920 925

Arg Glu Cys Leu Leu Ile Leu Asn Leu Lys Arg Lys Gln Lys Pro Ile
930 935 940

Leu Phe Phe Leu His Cys Ile Lys Lys Leu Asn Glu Gln Ala Ala
945 950 955 960

Glu Leu Phe Glu Ser Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile
965 970 975

Ile Met Asn Glu Phe Ile Val Pro Phe Leu Pro Leu Leu Leu Val Asp
980 985 990

Glu Met Glu Glu Lys Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg

995

1000

1005

Trp Cys Ser Tyr Leu Gly Gln Glu Met Glu Pro His Leu Gln Glu
1010 1015 1020

Lys Leu Thr Asp Phe Leu Pro Lys Leu Leu Asp Cys Ser Met Glu
1025 1030 1035

Ile Lys Ser Phe His Glu Pro Pro Lys Leu Pro Ser Tyr Ser Thr
1040 1045 1050

His Glu Leu Cys Glu Arg Phe Ala Arg Ile Met Leu Ser Leu Ser
1055 1060 1065

Arg Thr Pro Ala Asp Gly Arg
1070 1075